

Sequence Listing

<110> Kyoto University

<120> Cleaved forms of DANCE and DANCE complexes, and methods of screening an agent for regulating formation of elastic fibre using them

<130>

<150> JP 2004-096685

<151> 2004-3-29

<160> 29

<170> PatentIn version 3.2

<210> 1

<211> 1347

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1).. (1347)

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ctt cca agc cct ggg aat gca cag gca cag tgc acg aat ggc ttt gac	96
Leu Pro Ser Pro Gly Asn Ala Gln Ala Gln Cys Thr Asn Gly Phe Asp	
20 25 30	
ctg gat cgc cag tca gga cag tgt tta gat att gat gaa tgc cga acc	144
Leu Asp Arg Gln Ser Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Thr	
35 40 45	
atc ccc gag gcc tgc cga gga gac atg atg tgt gtt aac caa aat ggc	192
Ile Pro Glu Ala Cys Arg Gly Asp Met Met Cys Val Asn Gln Asn Gly	
50 55 60	
ggg tat tta tgc att ccc cgg aca aac cct gtg tat cga ggg ccc tac	240
Gly Tyr Leu Cys Ile Pro Arg Thr Asn Pro Val Tyr Arg Gly Pro Tyr	
65 70 75 80	
tcg aac ccc tac tgc acc ccc tac tca ggt cgg tac cca gca gct gcc	288
Ser Asn Pro Tyr Ser Thr Pro Tyr Ser Gly Pro Tyr Pro Ala Ala Ala	
85 90 95	
cca cca ctc tca gct cca aac tat ccc acg atc tcc agg cct ctt ata	336
Pro Pro Leu Ser Ala Pro Asn Tyr Pro Thr Ile Ser Arg Pro Leu Ile	
100 105 110	
tgc cgc ttt gga tac cag atg gat gaa agc aac caa tgt gtg gat gtg	384
Cys Arg Phe Gly Tyr Gln Met Asp Glu Ser Asn Gln Cys Val Asp Val	
115 120 125	
gac gag tgt gca aca gat tcc cac cag tgc aac ccc acc cag atc tgc	432
Asp Glu Cys Ala Thr Asp Ser His Gln Cys Asn Pro Thr Gln Ile Cys	
130 135 140	
atc aat act gaa ggc ggg tac acc tgc tcc tgc acc gac gga tat tgg	480
Ile Asn Thr Glu Gly Gly Tyr Thr Cys Ser Cys Thr Asp Gly Tyr Trp	
145 150 155 160	
ctt ctg gaa ggc cag tgc tta gac att gat gaa tgt cgc tat ggt tac	528
Leu Leu Glu Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Tyr Gly Tyr	
165 170 175	
tgc cag cag ctc tgt ggc aat gtt cct gga tcc tat tct tgt aca tgc	576
Cys Gln Gln Leu Cys Ala Asn Val Pro Gly Ser Tyr Ser Cys Thr Cys	
180 185 190	
aac cct ggt ttt acc ctc aat gag gat gga agg tct tgc caa gat gtg	624

Sequence Listing															
Asn	Pro	Gly	Phe	Thr	Leu	Asn	Glu	Asp	Gly	Arg	Ser	Cys	Gln	Asp	Val
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aac	gag	tgt	gcc	acc	gag	aac	ccc	tgc	gtg	caa	acc	tgc	gtc	aac	acc
Asn	Glu	Cys	Ala	Thr	Glu	Asn	Pro	Cys	Val	Gln	Thr	Cys	Val	Asn	Thr
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tac	ggc	tct	ttc	atc	tgc	cgc	tgt	gac	cca	gga	tat	gaa	ctt	gag	gaa
Tyr	Gly	Ser	Phe	Ile	Cys	Arg	Cys	Asp	Pro	Gly	Tyr	Glu	Leu	Glu	Glu
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gat	ggc	gtt	cat	tgc	agt	gat	atg	gac	gag	tgc	agc	ttc	tct	gag	ttc
Asp	Gly	Val	His	Cys	Ser	Asp	Met	Asp	Glu	Cys	Ser	Phe	Ser	Glu	Phe
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ctc	tgc	caa	cat	gag	tgt	gtg	aac	cag	ccc	ggc	aca	tac	ttc	tgc	tcc
Leu	Cys	Gln	His	Glu	Cys	Val	Asn	Gln	Pro	Gly	Thr	Tyr	Phe	Cys	Ser
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tgc	cct	cca	ggc	tac	atc	ctg	ctg	gat	gac	aac	cga	agc	tgc	caa	gac
Cys	Pro	Pro	Gly	Tyr	Ile	Leu	Leu	Asp	Asp	Asn	Arg	Ser	Cys	Gln	Asp
<div style="display: flex; justify-content: space-between;"> 275 280 285 </div>															
atc	aac	gaa	tgt	gag	cac	agg	aac	cac	acg	tgc	aac	ctg	cag	cag	acg
Ile	Asn	Glu	Cys	Glu	His	Arg	Asn	His	Thr	Cys	Asn	Leu	Gln	Gln	Thr
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tgc	tac	aat	tta	caa	ggg	ggc	ttc	aaa	tgc	atc	gac	ccc	atc	cgc	tgt
Cys	Tyr	Asn	Leu	Gln	Gly	Gly	Phe	Lys	Cys	Ile	Asp	Pro	Ile	Arg	Cys
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gag	gag	cct	tat	ctg	agg	atc	agt	gat	aac	cgc	tgt	atg	tgt	cct	gct
Glu	Glu	Pro	Tyr	Leu	Arg	Ile	Ser	Asp	Asn	Arg	Cys	Met	Cys	Pro	Ala
<div style="display: flex; justify-content: space-between;"> 325 330 335 </div>															
gag	aac	cct	ggc	tgc	aga	gac	cag	ccc	ttt	acc	atc	ttg	tac	cgg	gac
Glu	Asn	Pro	Gly	Cys	Arg	Asp	Gln	Pro	Phe	Thr	Ile	Leu	Tyr	Arg	Asp
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atg	gac	gtg	gtg	tca	gga	cgc	tcc	gtt	ccc	gct	gac	atc	ttc	caa	atg
Met	Asp	Val	Val	Ser	Gly	Arg	Ser	Val	Pro	Ala	Asp	Ile	Phe	Gln	Met
<div style="display: flex; justify-content: space-between;"> 355 360 365 </div>															
caa	gcc	acg	acc	cgc	tac	cct	ggg	gcc	tat	tac	att	ttc	cag	atc	aaa
Gln	Ala	Thr	Thr	Arg	Tyr	Pro	Gly	Ala	Tyr	Tyr	Ile	Phe	Gln	Ile	Lys
<div style="display: flex; justify-content: space-between;"> 370 375 380 </div>															
tct	ggg	aat	gag	ggc	aga	gaa	ttt	tac	atg	cgg	caa	acg	ggc	ccc	atc
Ser	Gly	Asn	Glu	Gly	Arg	Glu	Phe	Tyr	Met	Arg	Gln	Thr	Gly	Pro	Ile
<div style="display: flex; justify-content: space-between;"> 385 390 395 </div>															
agt	gcc	acc	ctg	gtg	atg	aca	cgc	ccc	atc	aaa	ggg	ccc	cgg	gaa	atc
Ser	Ala	Thr	Leu	Val	Met	Thr	Arg	Pro	Ile	Lys	Gly	Pro	Arg	Glu	Ile
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cag	ctg	gac	ttg	gaa	atg	atc	act	gtc	aac	act	gtc	atc	aac	ttc	aga
Gln	Leu	Asp	Leu	Glu	Met	Ile	Thr	Val	Asn	Thr	Val	Ile	Asn	Phe	Arg
<div style="display: flex; justify-content: space-between;"> 420 425 430 </div>															
ggc	agc	tcc	gtg	atc	cga	ctg	cgg	ata	tat	gtg	tgc	cag	tac	cca	ttc
Gly	Ser	Ser	Val	Ile	Arg	Leu	Arg	Ile	Tyr	Val	Ser	Gln	Tyr	Pro	Phe
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tga
1347

<210> 2
 <211> 448
 <212> PRT
 <213> Homo sapiens
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Met Pro Gly Ile Lys Arg Ile Leu Thr Val Thr Ile Leu Ala Leu Cys
 1 5 10 15

Sequence Listing

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 20 25 30
 Leu Asp Arg Gln Ser Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Thr
 35 40 45
 Ile Pro Glu Ala Cys Arg Gly Asp Met Met Cys Val Asn Gln Asn Gly
 50 55 60
 Gly Tyr Leu Cys Ile Pro Arg Thr Asn Pro Val Tyr Arg Gly Pro Tyr
 65 70 75 80
 Ser Asn Pro Tyr Ser Thr Pro Tyr Ser Gly Pro Tyr Pro Ala Ala Ala
 85 90 95
 Pro Pro Leu Ser Ala Pro Asn Tyr Pro Thr Ile Ser Arg Pro Leu Ile
 100 105 110
 Cys Arg Phe Gly Tyr Gln Met Asp Glu Ser Asn Gln Cys Val Asp Val
 115 120 125
 Asp Glu Cys Ala Thr Asp Ser His Gln Cys Asn Pro Thr Gln Ile Cys
 130 135 140
 Ile Asn Thr Glu Gly Gly Tyr Thr Cys Ser Cys Thr Asp Gly Tyr Trp
 145 150 155 160
 Leu Leu Glu Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Tyr Gly Tyr
 165 170 175
 Cys Gln Gln Leu Cys Ala Asn Val Pro Gly Ser Tyr Ser Cys Thr Cys
 180 185 190
 Asn Pro Gly Phe Thr Leu Asn Glu Asp Gly Arg Ser Cys Gln Asp Val
 195 200 205
 Asn Glu Cys Ala Thr Glu Asn Pro Cys Val Gln Thr Cys Val Asn Thr
 210 215 220
 Tyr Gly Ser Phe Ile Cys Arg Cys Asp Pro Gly Tyr Glu Leu Glu Glu
 225 230 235 240
 Asp Gly Val His Cys Ser Asp Met Asp Glu Cys Ser Phe Ser Glu Phe
 245 250 255
 Leu Cys Gln His Glu Cys Val Asn Gln Pro Gly Thr Tyr Phe Cys Ser
 260 265 270
 Cys Pro Pro Gly Tyr Ile Leu Leu Asp Asp Asn Arg Ser Cys Gln Asp
 275 280 285
 Ile Asn Glu Cys Glu His Arg Asn His Thr Cys Asn Leu Gln Gln Thr
 290 295 300
 Cys Tyr Asn Leu Gln Gly Gly Phe Lys Cys Ile Asp Pro Ile Arg Cys
 305 310 315 320

Sequence Listing

Glu Glu Pro Tyr Leu Arg Ile Ser Asp Asn Arg Cys Met Cys Pro Ala
325 330 335

Glu Asn Pro Gly Cys Arg Asp Gln Pro Phe Thr Ile Leu Tyr Arg Asp
340 345 350

Met Asp Val Val Ser Gly Arg Ser Val Pro Ala Asp Ile Phe Gln Met
355 360 365

Gln Ala Thr Thr Arg Tyr Pro Gly Ala Tyr Tyr Ile Phe Gln Ile Lys
370 375 380

Ser Gly Asn Glu Gly Arg Glu Phe Tyr Met Arg Gln Thr Gly Pro Ile
385 390 395 400

Ser Ala Thr Leu Val Met Thr Arg Pro Ile Lys Gly Pro Arg Glu Ile
405 410 415

Gln Leu Asp Leu Glu Met Ile Thr Val Asn Thr Val Ile Asn Phe Arg
420 425 430

Gly Ser Ser Val Ile Arg Leu Arg Ile Tyr Val Ser Gln Tyr Pro Phe
435 440 445

<210> 3
<211> 1278
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1).. (1278)

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1 5 10 15
tgt tta gat att gat gaa tgc cga acc atc ccc gag gcc tgc cga gga 96
Cys Leu Asp Ile Asp Glu Cys Arg Thr Ile Pro Glu Ala Cys Arg Gly
20 25 30
gac atg atg tgt gtt aac caa aat ggc ggg tat tta tgc att ccc cgg 144
Asp Met Met Cys Val Asn Gln Asn Gly Gly Tyr Leu Cys Ile Pro Arg
35 40 45
aca aac cct gtg tat cga ggg ccc tac tgc aac ccc tac tgc acc ccc 192
Thr Asn Pro Val Tyr Arg Gly Pro Tyr Ser Asn Pro Tyr Ser Thr Pro
50 55 60
tac tca ggt ccg tac cca gca gct gcc cca cca ctc tca gct cca aac 240
Tyr Ser Gly Pro Tyr Pro Ala Ala Ala Pro Pro Leu Ser Ala Pro Asn
65 70 75 80
tat ccc acg atc tcc agg cct ott ata tgc cgc ttt gga tac cag atg 288
Tyr Pro Thr Ile Ser Arg Pro Leu Ile Cys Arg Phe Gly Tyr Gln Met
85 90 95
gat gaa agc aac caa tgt gtg gat gtg gac gag tgt gca aca gat tcc 336
Asp Glu Ser Asn Gln Cys Val Asp Val Asp Glu Cys Ala Thr Asp Ser
100 105 110
cac cag tgc aac ccc acc cag atc tgc atc aat act gaa ggc ggg tac 384
His Gln Cys Asn Pro Thr Gln Ile Cys Ile Asn Thr Glu Gly Gly Tyr
115 120 125

Sequence Listing

acc tgc tcc tgc acc gac gga tat tgg ctt ctg gaa ggc cag tgc tta Thr Cys Ser Cys Thr Asp Gly Tyr Trp Leu Leu Glu Gly Gln Cys Leu 130 135 140	432
gac att gat gaa tgt cgc tat ggt tac tgc cag cag ctc tgt gcg aat Asp Ile Asp Glu Cys Arg Tyr Gly Tyr Cys Gln Gln Leu Cys Ala Asn 145 150 155 160	480
gtt cct gga tcc tat tot tgt aca tgc aac cct ggt ttt acc ctc aat Val Pro Gly Ser Tyr Ser Cys Thr Cys Asn Pro Gly Phe Thr Leu Asn 165 170 175	528
gag gat gga agg tct tgc caa gat gtg aac gag tgt gcc acc gag aac Glu Asp Gly Arg Ser Cys Gln Asp Val Asn Glu Cys Ala Thr Glu Asn 180 185 190	576
ccc tgc gtg caa acc tgc gtc aac acc tac ggc tct ttc atc tgc cgc Pro Cys Val Gln Thr Cys Val Asn Thr Tyr Gly Ser Phe Ile Cys Arg 195 200 205	624
tgt gac cca gga tat gaa ctt gag gaa gat ggc gtt cat tgc agt gat Cys Asp Pro Gly Tyr Glu Leu Glu Glu Asp Gly Val His Cys Ser Asp 210 215 220	672
atg gac gag tgc agc ttc tct gag ttc ctc tgc caa cat gag tgt gtg Met Asp Glu Cys Ser Phe Ser Glu Phe Leu Cys Gln His Glu Cys Val 225 230 235 240	720
aac cag ccc ggc aca tac ttc tgc tcc tgc cct cca ggc tac atc ctg Asn Gln Pro Gly Thr Tyr Phe Cys Ser Cys Pro Pro Gly Tyr Ile Leu 245 250 255	768
ctg gat gac aac cga agc tgc caa gac atc aac gaa tgt gag cac agg Leu Asp Asp Asn Arg Ser Cys Gln Asp Ile Asn Glu Cys Glu His Arg 260 265 270	816
aac cac acg tgc aac ctg cag cag acg tgc tac aat tta caa ggg ggc Asn His Thr Cys Asn Leu Gln Gln Thr Cys Tyr Asn Leu Gln Gly Gly 275 280 285	864
ttc aaa tgc atc gac ccc atc cgc tgt gag gag cct tat ctg agg atc Phe Lys Cys Ile Asp Pro Ile Arg Cys Glu Glu Pro Tyr Leu Arg Ile 290 295 300	912
agt gat aac cgc tgt atg tgt cct gct gag aac cct ggc tgc aga gac Ser Asp Asn Arg Cys Met Cys Pro Ala Glu Asn Pro Gly Cys Arg Asp 305 310 315 320	960
cag ccc ttt acc atc ttg tac cgg gac atg gac gtg gtg tca gga cgc Gln Pro Phe Thr Ile Leu Tyr Arg Asp Met Asp Val Val Ser Gly Arg 325 330 335	1008
tcc gtt ccc gct gac atc ttc caa atg caa gcc acg acc cgc tac cct Ser Val Pro Ala Asp Ile Phe Gln Met Gln Ala Thr Thr Arg Tyr Pro 340 345 350	1056
ggg gcc tat tac att ttc cag atc aaa tot ggg aat gag ggc aga gaa Gly Ala Tyr Tyr Ile Phe Gln Ile Lys Ser Gly Asn Glu Gly Arg Glu 355 360 365	1104
ttt tac atg cgg caa acg ggc ccc atc agt gcc acc ctg gtg atg aca Phe Tyr Met Arg Gln Thr Gly Pro Ile Ser Ala Thr Leu Val Met Thr 370 375 380	1152
cgc ccc atc aaa ggg ccc cgg gaa atc cag ctg gac ttg gaa atg atc Arg Pro Ile Lys Gly Pro Arg Glu Ile Gln Leu Asp Leu Glu Met Ile 385 390 395 400	1200
act gtc aac act gtc atc aac ttc aga ggc agc tcc gtg atc cga ctg Thr Val Asn Thr Val Ile Asn Phe Arg Gly Ser Ser Val Ile Arg Leu 405 410 415	1248
ogg ata tat gtg tgc cag tac cca ttc tga Arg Ile Tyr Val Ser Gln Tyr Pro Phe 420 425	1278

Sequence Listing

<210> 4
 <211> 425
 <212> PRT
 <213> Homo sapiens

<400> 4

Gln Ala Gln Cys Thr Asn Gly Phe Asp Leu Asp Arg Gln Ser Gly Gln
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Cys Leu Asp Ile Asp Glu Cys Arg Thr Ile Pro Glu Ala Cys Arg Gly
 20 25 30

Asp Met Met Cys Val Asn Gln Asn Gly Gly Tyr Leu Cys Ile Pro Arg
 35 40 45

Thr Asn Pro Val Tyr Arg Gly Pro Tyr Ser Asn Pro Tyr Ser Thr Pro
 50 55 60

Tyr Ser Gly Pro Tyr Pro Ala Ala Ala Pro Pro Leu Ser Ala Pro Asn
 65 70 75 80

Tyr Pro Thr Ile Ser Arg Pro Leu Ile Cys Arg Phe Gly Tyr Gln Met
 85 90 95

Asp Glu Ser Asn Gln Cys Val Asp Val Asp Glu Cys Ala Thr Asp Ser
 100 105 110

His Gln Cys Asn Pro Thr Gln Ile Cys Ile Asn Thr Glu Gly Gly Tyr
 115 120 125

Thr Cys Ser Cys Thr Asp Gly Tyr Trp Leu Leu Glu Gly Gln Cys Leu
 130 135 140

Asp Ile Asp Glu Cys Arg Tyr Gly Tyr Cys Gln Gln Leu Cys Ala Asn
 145 150 155 160

Val Pro Gly Ser Tyr Ser Cys Thr Cys Asn Pro Gly Phe Thr Leu Asn
 165 170 175

Glu Asp Gly Arg Ser Cys Gln Asp Val Asn Glu Cys Ala Thr Glu Asn
 180 185 190

Pro Cys Val Gln Thr Cys Val Asn Thr Tyr Gly Ser Phe Ile Cys Arg
 195 200 205

Cys Asp Pro Gly Tyr Glu Leu Glu Glu Asp Gly Val His Cys Ser Asp
 210 215 220

Met Asp Glu Cys Ser Phe Ser Glu Phe Leu Cys Gln His Glu Cys Val
 225 230 235 240

Asn Gln Pro Gly Thr Tyr Phe Cys Ser Cys Pro Pro Gly Tyr Ile Leu
 245 250 255

Leu Asp Asp Asn Arg Ser Cys Gln Asp Ile Asn Glu Cys Glu His Arg
 260 265 270

Sequence Listing

Asn His Thr Cys Asn Leu Gln Gln Thr Cys Tyr Asn Leu Gln Gly Gly
275 280 285

Phe Lys Cys Ile Asp Pro Ile Arg Cys Glu Glu Pro Tyr Leu Arg Ile
290 295 300

Ser Asp Asn Arg Cys Met Cys Pro Ala Glu Asn Pro Gly Cys Arg Asp
305 310 315 320

Gln Pro Phe Thr Ile Leu Tyr Arg Asp Met Asp Val Val Ser Gly Arg
325 330 335

Ser Val Pro Ala Asp Ile Phe Gln Met Gln Ala Thr Thr Arg Tyr Pro
340 345 350

Gly Ala Tyr Tyr Ile Phe Gln Ile Lys Ser Gly Asn Glu Gly Arg Glu
355 360 365

Phe Tyr Met Arg Gln Thr Gly Pro Ile Ser Ala Thr Leu Val Met Thr
370 375 380

Arg Pro Ile Lys Gly Pro Arg Glu Ile Gln Leu Asp Leu Glu Met Ile
385 390 395 400

Thr Val Asn Thr Val Ile Asn Phe Arg Gly Ser Ser Val Ile Arg Leu
405 410 415

Arg Ile Tyr Val Ser Gln Tyr Pro Phe
420 425

<210> 5
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<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(162)

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1 5 10 15
tgt tta gat att gat gaa tgc cga acc atc ccc gag gcc tgc cga gga 96
Cys Leu Asp Ile Asp Glu Cys Arg Thr Ile Pro Glu Ala Cys Arg Gly
20 25 30
gac atg atg tgt gtt aac caa aat ggc ggg tat tta tgc att ccc cgg 144
Asp Met Met Cys Val Asn Gln Asn Gly Gly Tyr Leu Cys Ile Pro Arg
35 40 45
aca aac cct gtg tat cga 162
Thr Asn Pro Val Tyr Arg
50

<210> 6
<211> 54
<212> PRT
<213> Homo sapiens

<400> 6

Sequence Listing

Gln Ala Gln Cys Thr Asn Gly Phe Asp Leu Asp Arg Gln Ser Gly Gln
1 5 10 15

Cys Leu Asp Ile Asp Glu Cys Arg Thr Ile Pro Glu Ala Cys Arg Gly
20 25 30

Asp Met Met Cys Val Asn Gln Asn Gly Gly Tyr Leu Cys Ile Pro Arg
35 40 45

Thr Asn Pro Val Tyr Arg
50

<210> 7
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<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1116)

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Gly Pro Tyr Ser Asn Pro Tyr Ser Thr Pro Tyr Ser Gly Pro Tyr Pro
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gca gct gcc cca cca ctc tca gct cca aac tat ccc acg atc tcc agg 96
Ala Ala Ala Pro Pro Leu Ser Ala Pro Asn Tyr Pro Thr Ile Ser Arg
20 25 30
cct ctt ata tgc cgc ttt gga tac cag atg gat gaa agc aac caa tgt 144
Pro Leu Ile Cys Arg Phe Gly Tyr Gln Met Asp Glu Ser Asn Gln Cys
35 40 45
gtg gat gtg gac gag tgt gca aca gat tcc cac cag tgc aac ccc acc 192
Val Asp Val Asp Glu Cys Ala Thr Asp Ser His Gln Cys Asn Pro Thr
50 55 60
cag atc tgc atc aat act gaa ggc ggg tac acc tgc tcc tgc acc gac 240
Gln Ile Cys Ile Asn Thr Glu Gly Gly Tyr Thr Cys Ser Cys Thr Asp
65 70 75 80
gga tat tgg ctt ctg gaa ggc cag tgc tta gac att gat gaa tgt cgc 288
Gly Tyr Trp Leu Leu Glu Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg
85 90 95
tat ggt tac tgc cag cag ctc tgt ggc aat gtt cct gga tcc tat tct 336
Tyr Gly Tyr Cys Gln Gln Leu Cys Ala Asn Val Pro Gly Ser Tyr Ser
100 105 110
tgt aca tgc aac cct ggt ttt acc ctc aat gag gat gga agg tct tgc 384
Cys Thr Cys Asn Pro Gly Phe Thr Leu Asn Glu Asp Gly Arg Ser Cys
115 120 125
caa gat gtg aac gag tgt gcc acc gag aac ccc tgc gtg caa acc tgc 432
Gln Asp Val Asn Glu Cys Ala Thr Glu Asn Pro Cys Val Gln Thr Cys
130 135 140
gtc aac acc tac ggc tct ttc atc tgc cgc tgt gac cca gga tat gaa 480
Val Asn Thr Tyr Gly Ser Phe Ile Cys Arg Cys Asp Pro Gly Tyr Glu
145 150 155 160
ctt gag gaa gat ggc gtt cat tgc agt gat atg gac gag tgc agc ttc 528
Leu Glu Glu Asp Gly Val His Cys Ser Asp Met Asp Glu Cys Ser Phe
165 170 175
tct gag ttc ctc tgc caa cat gag tgt gtg aac cag ccc ggc aca tac 576
Ser Glu Phe Leu Cys Gln His Glu Cys Val Asn Gln Pro Gly Thr Tyr
180 185 190
ttc tgc tcc tgc cct cca ggc tac atc ctg ctg gat gac aac cga agc 624

Sequence Listing

Phe Cys Ser Cys Pro Pro Gly Tyr Ile Leu Leu Asp Asp Asn Arg Ser	
195 200 205	
tgc caa gac atc aac gaa tgt gag cac agg aac cac acg tgc aac ctg	672
Cys Gln Asp Ile Asn Glu Cys Glu His Arg Asn His Thr Cys Asn Leu	
210 215 220	
cag cag acg tgc tac aat tta caa ggg ggc ttc aaa tgc atc gac ccc	720
Gln Gln Thr Cys Tyr Asn Leu Gln Gly Gly Phe Lys Cys Ile Asp Pro	
225 230 235 240	
atc cgc tgt gag gag cct tat ctg agg atc agt gat aac cgc tgt atg	768
Ile Arg Cys Glu Glu Pro Tyr Leu Arg Ile Ser Asp Asn Arg Cys Met	
245 250 255	
tgt cct gct gag aac cct ggc tgc aga gac cag ccc ttt acc atc ttg	816
Cys Pro Ala Glu Asn Pro Gly Cys Arg Asp Gln Pro Phe Thr Ile Leu	
260 265 270	
tac cgg gac atg gac gtg gtg tca gga cgc tcc gtt ccc gct gac atc	864
Tyr Arg Asp Met Asp Val Val Ser Gly Arg Ser Val Pro Ala Asp Ile	
275 280 285	
ttc caa atg caa gcc acg acc cgc tac cct ggg gcc tat tac att ttc	912
Phe Gln Met Gln Ala Thr Thr Arg Tyr Pro Gly Ala Tyr Tyr Ile Phe	
290 295 300	
cag atc aaa tct ggg aat gag ggc aga gaa ttt tac atg cgg caa acg	960
Gln Ile Lys Ser Gly Asn Glu Gly Arg Glu Phe Tyr Met Arg Gln Thr	
305 310 315 320	
ggc ccc atc agt gcc acc ctg gtg atg aca cgc ccc atc aaa ggg ccc	1008
Gly Pro Ile Ser Ala Thr Leu Val Met Thr Arg Pro Ile Lys Gly Pro	
325 330 335	
cgg gaa atc cag ctg gac ttg gaa atg atc act gtc aac act gtc atc	1056
Arg Glu Ile Gln Leu Asp Leu Glu Met Ile Thr Val Asn Thr Val Ile	
340 345 350	
aac ttc aga ggc ago tcc gtg atc cga ctg cgg ata tat gtg tgc cag	1104
Asn Phe Arg Gly Ser Ser Val Ile Arg Leu Arg Ile Tyr Val Ser Gln	
355 360 365	
tac cca ttc tga	1116
Tyr Pro Phe	
370	

<210> 8
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 <212> PRT
 <213> Homo sapiens

<400> 8

Gly Pro Tyr Ser Asn Pro Tyr Ser Thr Pro Tyr Ser Gly Pro Tyr Pro	
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Ala Ala Ala Pro Pro Leu Ser Ala Pro Asn Tyr Pro Thr Ile Ser Arg	
20 25 30	
Pro Leu Ile Cys Arg Phe Gly Tyr Gln Met Asp Glu Ser Asn Gln Cys	
35 40 45	
Val Asp Val Asp Glu Cys Ala Thr Asp Ser His Gln Cys Asn Pro Thr	
50 55 60	
Gln Ile Cys Ile Asn Thr Glu Gly Gly Tyr Thr Cys Ser Cys Thr Asp	
65 70 75 80	
Gly Tyr Trp Leu Leu Glu Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg	

Sequence Listing
95

85

90

Tyr Gly Tyr Cys Gln Gln Leu Cys Ala Asn Val Pro Gly Ser Tyr Ser
100 105 110

Cys Thr Cys Asn Pro Gly Phe Thr Leu Asn Glu Asp Gly Arg Ser Cys
115 120 125

Gln Asp Val Asn Glu Cys Ala Thr Glu Asn Pro Cys Val Gln Thr Cys
130 135 140

Val Asn Thr Tyr Gly Ser Phe Ile Cys Arg Cys Asp Pro Gly Tyr Glu
145 150 155 160

Leu Glu Glu Asp Gly Val His Cys Ser Asp Met Asp Glu Cys Ser Phe
165 170 175

Ser Glu Phe Leu Cys Gln His Glu Cys Val Asn Gln Pro Gly Thr Tyr
180 185 190

Phe Cys Ser Cys Pro Pro Gly Tyr Ile Leu Leu Asp Asp Asn Arg Ser
195 200 205

Cys Gln Asp Ile Asn Glu Cys Glu His Arg Asn His Thr Cys Asn Leu
210 215 220

Gln Gln Thr Cys Tyr Asn Leu Gln Gly Gly Phe Lys Cys Ile Asp Pro
225 230 235 240

Ile Arg Cys Glu Glu Pro Tyr Leu Arg Ile Ser Asp Asn Arg Cys Met
245 250 255

Cys Pro Ala Glu Asn Pro Gly Cys Arg Asp Gln Pro Phe Thr Ile Leu
260 265 270

Tyr Arg Asp Met Asp Val Val Ser Gly Arg Ser Val Pro Ala Asp Ile
275 280 285

Phe Gln Met Gln Ala Thr Thr Arg Tyr Pro Gly Ala Tyr Tyr Ile Phe
290 295 300

Gln Ile Lys Ser Gly Asn Glu Gly Arg Glu Phe Tyr Met Arg Gln Thr
305 310 315 320

Gly Pro Ile Ser Ala Thr Leu Val Met Thr Arg Pro Ile Lys Gly Pro
325 330 335

Arg Glu Ile Gln Leu Asp Leu Glu Met Ile Thr Val Asn Thr Val Ile
340 345 350

Asn Phe Arg Gly Ser Ser Val Ile Arg Leu Arg Ile Tyr Val Ser Gln
355 360 365

Tyr Pro Phe
370

<210> 9

Sequence Listing

<211> 162
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(162)

<400> 9
cag cag cag tgc aca aac ggc ttt gac ctg gac cgc cag tca gga cag 48
Gln Gln Gln Cys Thr Asn Gly Phe Asp Leu Asp Arg Gln Ser Gly Gln
1 5 10 15
tgt cta gat att gat gaa tgc cgg acc atc cct gag gct tgt cgt ggg 96
Cys Leu Asp Ile Asp Glu Cys Arg Thr Ile Pro Glu Ala Cys Arg Gly
20 25 30
gac atg atg tgt gtc aac cag aat ggc ggg tat ttg tgc atc cct cga 144
Asp Met Met Cys Val Asn Gln Asn Gly Gly Tyr Leu Cys Ile Pro Arg
35 40 45
acc aac cca gtg tat cga 162
Thr Asn Pro Val Tyr Arg
50

<210> 10
<211> 54
<212> PRT
<213> Mus musculus

<400> 10
Gln Gln Gln Cys Thr Asn Gly Phe Asp Leu Asp Arg Gln Ser Gly Gln
1 5 10 15
Cys Leu Asp Ile Asp Glu Cys Arg Thr Ile Pro Glu Ala Cys Arg Gly
20 25 30
Asp Met Met Cys Val Asn Gln Asn Gly Gly Tyr Leu Cys Ile Pro Arg
35 40 45
Thr Asn Pro Val Tyr Arg
50

<210> 11
<211> 1113
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(1113)

<400> 11
ggg cct tac tca aat ccc tac tct aca tcc tac tca ggc cca tac cca 48
Gly Pro Tyr Ser Asn Pro Tyr Ser Thr Ser Tyr Ser Gly Pro Tyr Pro
1 5 10 15
gca gcg gcc cca cca gta cca gct tcc aac tac ccc acg att tca agg 96
Ala Ala Ala Pro Pro Val Pro Ala Ser Asn Tyr Pro Thr Ile Ser Arg
20 25 30
cct ctt gtc tgc cgc ttt ggg tat cag atg gat gaa ggc aac cag tgt 144
Pro Leu Val Cys Arg Phe Gly Tyr Gln Met Asp Glu Gly Asn Gln Cys
35 40 45
gtg gat gtg gac gag tgt gca aca gac tca cac cag tgc aac cct acc 192
Val Asp Val Asp Glu Cys Ala Thr Asp Ser His Gln Cys Asn Pro Thr
50 55 60

Sequence Listing

cag atc tgt atc aac act gaa gga ggt tac acc tgc tcc tgc acc gat Gln Ile Cys Ile Asn Thr Glu Gly Gly Tyr Thr Cys Ser Cys Thr Asp 65 70 75 80	240
ggg tac tgg ctt ctg gaa ggg cag tgc cta gat att gat gaa tgt cgc Gly Tyr Trp Leu Leu Glu Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg 85 90 95	288
tat ggt tac tgc cag cag ctc tgt gca aat gtt cca gga tcc tat tcc Tyr Gly Tyr Cys Gln Gln Leu Cys Ala Asn Val Pro Gly Ser Tyr Ser 100 105 110	336
tgt aca tgc aac cct ggt ttc acc ctc aac gac gat gga agg tot tgc Cys Thr Cys Asn Pro Gly Phe Thr Leu Asn Asp Asp Gly Arg Ser Cys 115 120 125	384
caa gat gtg aac gag tgc gaa act gag aat ccc tgt gtt cag acc tgt Gln Asp Val Asn Glu Cys Glu Thr Glu Asn Pro Cys Val Gln Thr Cys 130 135 140	432
gtc aac acc tat ggc tot ttc atc tgc cgc tgt gac cca gga tat gaa Val Asn Thr Tyr Gly Ser Phe Ile Cys Arg Cys Asp Pro Gly Tyr Glu 145 150 155 160	480
ctt gag gaa gat ggc att cac tgc agt gat atg gac gag tgc ago ttc Leu Glu Glu Asp Gly Ile His Cys Ser Asp Met Asp Glu Cys Ser Phe 165 170 175	528
tcc gag ttc ctc tgt caa cac gag tgt gtg aac cag ccg ggc tca tac Ser Glu Phe Leu Cys Gln His Glu Cys Val Asn Gln Pro Gly Ser Tyr 180 185 190	576
ttc tgc tgc tgc cct cca ggc tac gtc ctg ttg gat gat aac cga agc Phe Cys Ser Cys Pro Pro Gly Tyr Val Leu Leu Asp Asp Asn Arg Ser 195 200 205	624
tgc cag gat atc aat gaa tgt gag cac cga aac cac acg tgt acc tca Cys Gln Asp Ile Asn Glu Cys Glu His Arg Asn His Thr Cys Thr Ser 210 215 220	672
ctg cag act tgc tac aat cta caa ggg ggc ttc aaa tgt att gat ccc Leu Gln Thr Cys Tyr Asn Leu Gln Gly Gly Phe Lys Cys Ile Asp Pro 225 230 235 240	720
atc agc tgt gag gag cct tat ctg ctg att ggt gaa aac cgc tgt atg Ile Ser Cys Glu Glu Pro Tyr Leu Leu Ile Gly Glu Asn Arg Cys Met 245 250 255	768
tgt cct gct gag cac acc agc tgc aga gac cag cca ttc acc atc ctg Cys Pro Ala Glu His Thr Ser Cys Arg Asp Gln Pro Phe Thr Ile Leu 260 265 270	816
tat cgg gac atg gat gtg gtg tca gga cgc tcc gtt cct gct gac atc Tyr Arg Asp Met Asp Val Val Ser Gly Arg Ser Val Pro Ala Asp Ile 275 280 285	864
ttc cag atg caa gca aca acc cga tac cct ggt gcc tat tac att ttc Phe Gln Met Gln Ala Thr Thr Arg Tyr Pro Gly Ala Tyr Tyr Ile Phe 290 295 300	912
cag atc aaa tct ggc aac gag ggt cga gag ttc tat atg cgg caa aca Gln Ile Lys Ser Gly Asn Glu Gly Arg Glu Phe Tyr Met Arg Gln Thr 305 310 315 320	960
ggg cct atc agt gcc acc ctg gtg atg aca cgc ccc atc aaa ggg cct Gly Pro Ile Ser Ala Thr Leu Val Met Thr Arg Pro Ile Lys Gly Pro 325 330 335	1008
cgg gac atc cag ctg gac ttg gag atg atc act gtc aac act gtc atc Arg Asp Ile Gln Leu Asp Leu Glu Met Ile Thr Val Asn Thr Val Ile 340 345 350	1056
aac ttc aga ggc agc tcc gtg atc cga ctg cgg ata tat gtg tgc cag Asn Phe Arg Gly Ser Ser Val Ile Arg Leu Arg Ile Tyr Val Ser Gln 355 360 365	1104

Sequence Listing

1113

tat ccg ttc
Tyr Pro Phe
370

<210> 12
<211> 371
<212> PRT
<213> Mus musculus

<400> 12

Gly Pro Tyr Ser Asn Pro Tyr Ser Thr Ser Tyr Ser Gly Pro Tyr Pro
1 5 10 15

Ala Ala Ala Pro Pro Val Pro Ala Ser Asn Tyr Pro Thr Ile Ser Arg
20 25 30

Pro Leu Val Cys Arg Phe Gly Tyr Gln Met Asp Glu Gly Asn Gln Cys
35 40 45

Val Asp Val Asp Glu Cys Ala Thr Asp Ser His Gln Cys Asn Pro Thr
50 55 60

Gln Ile Cys Ile Asn Thr Glu Gly Gly Tyr Thr Cys Ser Cys Thr Asp
65 70 75 80

Gly Tyr Trp Leu Leu Glu Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg
85 90 95

Tyr Gly Tyr Cys Gln Gln Leu Cys Ala Asn Val Pro Gly Ser Tyr Ser
100 105 110

Cys Thr Cys Asn Pro Gly Phe Thr Leu Asn Asp Asp Gly Arg Ser Cys
115 120 125

Gln Asp Val Asn Glu Cys Glu Thr Glu Asn Pro Cys Val Gln Thr Cys
130 135 140

Val Asn Thr Tyr Gly Ser Phe Ile Cys Arg Cys Asp Pro Gly Tyr Glu
145 150 155 160

Leu Glu Glu Asp Gly Ile His Cys Ser Asp Met Asp Glu Cys Ser Phe
165 170 175

Ser Glu Phe Leu Cys Gln His Glu Cys Val Asn Gln Pro Gly Ser Tyr
180 185 190

Phe Cys Ser Cys Pro Pro Gly Tyr Val Leu Leu Asp Asp Asn Arg Ser
195 200 205

Cys Gln Asp Ile Asn Glu Cys Glu His Arg Asn His Thr Cys Thr Ser
210 215 220

Leu Gln Thr Cys Tyr Asn Leu Gln Gly Gly Phe Lys Cys Ile Asp Pro
225 230 235 240

Ile Ser Cys Glu Glu Pro Tyr Leu Leu Ile Gly Glu Asn Arg Cys Met
245 250 255

Sequence Listing

Cys Pro Ala Glu His Thr Ser Cys Arg Asp Gln Pro Phe Thr Ile Leu
260 265 270

Tyr Arg Asp Met Asp Val Val Ser Gly Arg Ser Val Pro Ala Asp Ile
275 280 285

Phe Gln Met Gln Ala Thr Thr Arg Tyr Pro Gly Ala Tyr Tyr Ile Phe
290 295 300

Gln Ile Lys Ser Gly Asn Glu Gly Arg Glu Phe Tyr Met Arg Gln Thr
305 310 315 320

Gly Pro Ile Ser Ala Thr Leu Val Met Thr Arg Pro Ile Lys Gly Pro
325 330 335

Arg Asp Ile Gln Leu Asp Leu Glu Met Ile Thr Val Asn Thr Val Ile
340 345 350

Asn Phe Arg Gly Ser Ser Val Ile Arg Leu Arg Ile Tyr Val Ser Gln
355 360 365

Tyr Pro Phe
370

<210> 13
<211> 162
<212> DNA
<213> Rattus norvegicus

<220>
<221> CDS
<222> (1)..(162)

<400> 13
cag caa cag tgc acc aac ggc ttt gac ctg gac cgc cag aca gga cag 48
Gln Gln Gln Cys Thr Asn Gly Phe Asp Leu Asp Arg Gln Thr Gly Gln
1 5 10 15
tgt tta gat att gat gaa tgt cgg acc atc cct gag gct tgc cgt ggg 96
Cys Leu Asp Ile Asp Glu Cys Arg Thr Ile Pro Glu Ala Cys Arg Gly
20 25 30
gac atg atg tgt gtc aac cag aat ggc ggg tat ctg tgc atc cct cga 144
Asp Met Met Cys Val Asn Gln Asn Gly Gly Tyr Leu Cys Ile Pro Arg
35 40 45
acc aac cca gtg tat cga 162
Thr Asn Pro Val Tyr Arg
50

<210> 14
<211> 54
<212> PRT
<213> Rattus norvegicus

<400> 14

Gln Gln Gln Cys Thr Asn Gly Phe Asp Leu Asp Arg Gln Thr Gly Gln
1 5 10 15

Cys Leu Asp Ile Asp Glu Cys Arg Thr Ile Pro Glu Ala Cys Arg Gly
20 25 30

Sequence Listing

Asp Met Met Cys Val Asn Gln Asn Gly Gly Tyr Leu Cys Ile Pro Arg
 35 40 45

Thr Asn Pro Val Tyr Arg
 50

<210> 15
 <211> 1116
 <212> DNA
 <213> Rattus norvegicus

<220>
 <221> CDS
 <222> (1).. (1116)

<400> 15
 ggg ccc tac tcc aat ccc tac tct aca tcc tac tca ggc cca tac cca 48
 Gly Pro Tyr Ser Asn Pro Tyr Ser Thr Ser Tyr Ser Gly Pro Tyr Pro
 1 5 10 15

gca gcc gca cca cca gtg cca gct tcc aac tac ccc acg att tcc agg 96
 Ala Ala Ala Pro Pro Val Pro Ala Ser Asn Tyr Pro Thr Ile Ser Arg
 20 25 30

cct ctt gtc tgt cgc ttt ggg tat cag atg gat gaa ggc aac cag tgt 144
 Pro Leu Val Cys Arg Phe Gly Tyr Gln Met Asp Glu Gly Asn Gln Cys
 35 40 45

gtg gat gtg gac gag tgt gcg aca gat tca cac cag tgc aac cct acc 192
 Val Asp Val Asp Glu Cys Ala Thr Asp Ser His Gln Cys Asn Pro Thr
 50 55 60

cag atc tgt atc aac acg gaa gga ggg tac acc tgc tcc tgc act gat 240
 Gln Ile Cys Ile Asn Thr Glu Gly Gly Tyr Thr Cys Ser Cys Thr Asp
 65 70 75 80

ggg tac tgg ctt ctg gaa ggg cag tgc cta gat att gat gaa tgt cgc 288
 Gly Tyr Trp Leu Leu Glu Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg
 85 90 95

tat ggt tac tgc cag cag ctc tgt gcg aat gtt cct gga tcc tat tcc 336
 Tyr Gly Tyr Cys Gln Gln Leu Cys Ala Asn Val Pro Gly Ser Tyr Ser
 100 105 110

tgt acg tgt aac cct ggc ttc acc ctc aac gat gat gga agg tct tgc 384
 Cys Thr Cys Asn Pro Gly Phe Thr Leu Asn Asp Asp Gly Arg Ser Cys
 115 120 125

caa gat gtg aac gag tgt gaa act gag aac ccc tgt gtt cag acc tgc 432
 Gln Asp Val Asn Glu Cys Glu Thr Glu Asn Pro Cys Val Gln Thr Cys
 130 135 140

gtc aac acc tat ggt tct ttc atc tgc cgc tgt gac cca gga tat gaa 480
 Val Asn Thr Tyr Gly Ser Phe Ile Cys Arg Cys Asp Pro Gly Tyr Glu
 145 150 155 160

ctg gag gaa gat ggc att cac tgc agt gat atg gat gag tgc agc ttc 528
 Leu Glu Glu Asp Gly Ile His Cys Ser Asp Met Asp Glu Cys Ser Phe
 165 170 175

tcc gag ttc ctc tgt caa cat gag tgt gtg aac cag ccg ggc tca tac 576
 Ser Glu Phe Leu Cys Gln His Glu Cys Val Asn Gln Pro Gly Ser Tyr
 180 185 190

ttc tgc tca tgc cct cca ggc tac gtc ttg ttg gaa gat aac cga agc 624
 Phe Cys Ser Cys Pro Pro Gly Tyr Val Leu Leu Glu Asp Asn Arg Ser
 195 200 205

tgc cag gat atc aat gaa tgt gag cac cgg aac cac aca tgc act ccc 672
 Cys Gln Asp Ile Asn Glu Cys Glu His Arg Asn His Thr Cys Thr Pro
 210 215 220

ctg cag act tgc tac aat ctg caa ggg ggc ttc aaa tgt atc gac ccc 720

Sequence Listing

Leu Gln Thr Cys Tyr Asn Leu Gln Gly Gly Phe Lys Cys Ile Asp Pro	
225 230 235 240	
atc gtc tgc gag gag cct tat ctg ctg att ggg gat aac cgc tgt atg	768
Ile Val Cys Glu Glu Pro Tyr Leu Leu Ile Gly Asp Asn Arg Cys Met	
245 250 255	
tgc cct gct gag aat act ggc tgc agg gac cag cca ttc acc atc ttg	816
Cys Pro Ala Glu Asn Thr Gly Cys Arg Asp Gln Pro Phe Thr Ile Leu	
260 265 270	
ttt cgg gac atg gat gtg gta tca gga cgc tct gtt cct gct gac atc	864
Phe Arg Asp Met Asp Val Val Ser Gly Arg Ser Val Pro Ala Asp Ile	
275 280 285	
ttc cag atg caa gca acg acc cga tac cct ggc gcc tat tac att ttc	912
Phe Gln Met Gln Ala Thr Thr Arg Tyr Pro Gly Ala Tyr Tyr Ile Phe	
290 295 300	
cag atc aaa tct ggg aac gag ggt cga gag ttc tac atg cgg caa aca	960
Gln Ile Lys Ser Gly Asn Glu Gly Arg Glu Phe Tyr Met Arg Gln Thr	
305 310 315 320	
ggg cct atc agt gcc acc ctg gtg atg aca cgc ccc atc aaa ggg cct	1008
Gly Pro Ile Ser Ala Thr Leu Val Met Thr Arg Pro Ile Lys Gly Pro	
325 330 335	
cgg gac atc cag ctg gac ttg gag atg atc acc gtc aac act gtc atc	1056
Arg Asp Ile Gln Leu Asp Leu Glu Met Ile Thr Val Asn Thr Val Ile	
340 345 350	
aac ttc aga ggc agc tcc gtg atc cga ctg cgg ata tac gtg tcc cag	1104
Asn Phe Arg Gly Ser Ser Val Ile Arg Leu Arg Ile Tyr Val Ser Gln	
355 360 365	
tat ccg ttc tga	1116
Tyr Pro Phe	
370	

<210> 16
 <211> 371
 <212> PRT
 <213> Rattus norvegicus

<400> 16

Gly Pro Tyr Ser Asn Pro Tyr Ser Thr Ser Tyr Ser Gly Pro Tyr Pro	
1 5 10 15	
Ala Ala Ala Pro Pro Val Pro Ala Ser Asn Tyr Pro Thr Ile Ser Arg	
20 25 30	
Pro Leu Val Cys Arg Phe Gly Tyr Gln Met Asp Glu Gly Asn Gln Cys	
35 40 45	
Val Asp Val Asp Glu Cys Ala Thr Asp Ser His Gln Cys Asn Pro Thr	
50 55 60	
Gln Ile Cys Ile Asn Thr Glu Gly Gly Tyr Thr Cys Ser Cys Thr Asp	
65 70 75 80	
Gly Tyr Trp Leu Leu Glu Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg	
85 90 95	
Tyr Gly Tyr Cys Gln Gln Leu Cys Ala Asn Val Pro Gly Ser Tyr Ser	
100 105 110	
Cys Thr Cys Asn Pro Gly Phe Thr Leu Asn Asp Asp Gly Arg Ser Cys	

Sequence Listing

115

120

125

Gln Asp Val Asn Glu Cys Glu Thr Glu Asn Pro Cys Val Gln Thr Cys
130 135 140

Val Asn Thr Tyr Gly Ser Phe Ile Cys Arg Cys Asp Pro Gly Tyr Glu
145 150 155 160

Leu Glu Glu Asp Gly Ile His Cys Ser Asp Met Asp Glu Cys Ser Phe
165 170 175

Ser Glu Phe Leu Cys Gln His Glu Cys Val Asn Gln Pro Gly Ser Tyr
180 185 190

Phe Cys Ser Cys Pro Pro Gly Tyr Val Leu Leu Glu Asp Asn Arg Ser
195 200 205

Cys Gln Asp Ile Asn Glu Cys Glu His Arg Asn His Thr Cys Thr Pro
210 215 220

Leu Gln Thr Cys Tyr Asn Leu Gln Gly Gly Phe Lys Cys Ile Asp Pro
225 230 235 240

Ile Val Cys Glu Glu Pro Tyr Leu Leu Ile Gly Asp Asn Arg Cys Met
245 250 255

Cys Pro Ala Glu Asn Thr Gly Cys Arg Asp Gln Pro Phe Thr Ile Leu
260 265 270

Phe Arg Asp Met Asp Val Val Ser Gly Arg Ser Val Pro Ala Asp Ile
275 280 285

Phe Gln Met Gln Ala Thr Thr Arg Tyr Pro Gly Ala Tyr Tyr Ile Phe
290 295 300

Gln Ile Lys Ser Gly Asn Glu Gly Arg Glu Phe Tyr Met Arg Gln Thr
305 310 315 320

Gly Pro Ile Ser Ala Thr Leu Val Met Thr Arg Pro Ile Lys Gly Pro
325 330 335

Arg Asp Ile Gln Leu Asp Leu Glu Met Ile Thr Val Asn Thr Val Ile
340 345 350

Asn Phe Arg Gly Ser Ser Val Ile Arg Leu Arg Ile Tyr Val Ser Gln
355 360 365

Tyr Pro Phe
370

<210> 17
<211> 173
<212> DNA
<213> Artificial

<220>
<223> DNA encoding preprotrypsin signal peptide, FLAG tag, 6 x His tag
and restriction sites

Sequence Listing

<400> 17
 ggtaccgcta gccaattcac catgtctgca cttctgatcc tagctcttgt tggagctgca 60
 gttgctgact acaaagaaga tgacgacaag actagtcac atcaccatca ccattctaga 120
 gaaggatccg atatccgagg ccgcatcgat tgactagctg aggcgcgcaaa ccc 173

<210> 18
 <211> 15
 <212> PRT
 <213> Artificial

<220>
 <223> preprotrypsin signal peptide

<400> 18
 Met Ser Ala Leu Leu Ile Leu Ala Leu Val Gly Ala Ala Val Ala
 1 5 10 15

<210> 19
 <211> 8
 <212> PRT
 <213> Artificial

<220>
 <223> FLAG tag

<400> 19
 Asp Tyr Lys Asp Asp Asp Asp Lys
 1 5

<210> 20
 <211> 6
 <212> PRT
 <213> Artificial

<220>
 <223> 6 x His tag

<400> 20
 His His His His His His
 1 5

<210> 21
 <211> 105
 <212> DNA
 <213> Artificial

<220>
 <223> DNA encoding preprotrypsin signal peptide, Myc tag and restriction sites

<400> 21
 gaattcacca tgtctgcaact tctgatccta gctcttggtg gagctgcagt tgotgactac 60
 gaagaggacg acaaaaaact catctcagaa gaggatctga ctagt 105

<210> 22
 <211> 10
 <212> PRT
 <213> Artificial

<220>
 <223> Myc tag

<400> 22
 Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu

Sequence Listing

1	5	10	
<210>	23		
<211>	143		
<212>	DNA		
<213>	Artificial		
<220>			
<223>	DNA encoding FLAG tag, 6 x His tag and restriction sites		
<400>	23		
	tggtaccgag ctcggatcca ctagtccagt gtggtggaat tctgcagata tccagcacag	60	
	tggcgccgt ctagagacta caaagacgat gacgacaaga gagggctctca tcaccacat	120	
	caccattgag cggccgcaaa ccc	143	
<210>	24		
<211>	28		
<212>	DNA		
<213>	Artificial		
<220>			
<223>	PCR primer for amplifying human DANCE		
<400>	24		
	tctagagcac agtcacgaa tggctttg	28	
<210>	25		
<211>	38		
<212>	DNA		
<213>	Artificial		
<220>			
<223>	PCR primer for amplifying human DANCE		
<400>	25		
	gcggccggtc agaattggta ctgcgacaca tatatccg	38	
<210>	26		
<211>	33		
<212>	DNA		
<213>	Artificial		
<220>			
<223>	PCR primer for amplifying human LTBP2		
<400>	26		
	tctagacaaa gggaccccggt agggagatac gag	33	
<210>	27		
<211>	34		
<212>	DNA		
<213>	Artificial		
<220>			
<223>	PCR primer for amplifying human LTBP2		
<400>	27		
	gcggccgcct ggtactcott ggcagtgcag tggg	34	
<210>	28		
<211>	31		
<212>	DNA		
<213>	Artificial		
<220>			
<223>	PCR primer for amplifying human DANCE		
<400>	28		

Sequence Listing

gaattcttct tctgccttc gcattctctc c

31

<210> 29

<211> 33

<212> DNA

<213> Artificial

<220>

<223> PCR primer for amplifying human DANCE

<400> 29

tctagagaat gggtactgcg acacatatat ccg

33